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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/708,693 DATE: 11/27/2000
TIME: 09:28:08

Input Set : A:\JHU1120-15.ST25.txt
Output Set: N:\CRF3\11272000\I708693.raw

3 <110> APPLICANT: Johns Hopkins University School of Medicine
4 Se-Jin, Lee
5 Alexandra, McPherron
7 <120> TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING PROMYOSTATIN POLYPEPTIDES
9 <130> FILE REFERENCE: JHU1120-15
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/708,693
12 <141> CURRENT FILING DATE: 2000-11-07
14 <150> PRIOR APPLICATION NUMBER: 09/628,112
15 <151> PRIOR FILING DATE: 2000-07-27
17 <150> PRIOR APPLICATION NUMBER: 09/124,180
18 <151> PRIOR FILING DATE: 1998-07-28
20 <150> PRIOR APPLICATION NUMBER: 09/019,070
21 <151> PRIOR FILING DATE: 1998-02-05
23 <150> PRIOR APPLICATION NUMBER: 08/862,445
24 <151> PRIOR FILING DATE: 1997-05-23
26 <150> PRIOR APPLICATION NUMBER: 08/847,910
27 <151> PRIOR FILING DATE: 1997-04-28
29 <150> PRIOR APPLICATION NUMBER: 08/795,071
30 <151> PRIOR FILING DATE: 1997-02-05
32 <150> PRIOR APPLICATION NUMBER: 08/525,596
33 <151> PRIOR FILING DATE: 1995-10-26
35 <160> NUMBER OF SEQ ID NOS: 29
37 <170> SOFTWARE: PatentIn version 3.0
39 <210> SEQ ID NO: 1
40 <211> LENGTH: 2743
41 <212> TYPE: DNA
42 <213> ORGANISM: Homo sapiens
44 <220> FEATURE:
45 <221> NAME/KEY: CDS
46 <222> LOCATION: (59)..(1183)
48 <400> SEQUENCE: 1
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51 atg caa aaa ctg caa ctc tgt gtt tat att tac ctg ttt atg ctg att 106
52 Met Gln Lys Leu Gln Leu Cys Val Tyr Ile Tyr Leu Phe Met Leu Ile
53 1 5 10 15
55 gtt gct ggt cca gtg gat cta aat gag aac agt gag caa aaa gaa aat 154
56 Val Ala Gly Pro Val Asp Leu Asn Glu Asn Ser Glu Gln Lys Glu Asn
57 20 25 30
59 gtg gaa aaa gag ggg ctg tgt aat gca tgt act tgg aga caa aac act 202
60 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
61 35 40 45
63 aaa tct tca aga ata gaa gcc att aag ata caa atc ctc agt aaa ctt 250
64 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
65 50 55 60
67 cgt ctg gaa aca gct cct aac atc agc aaa gat gtt ata aga caa ctt 298
68 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
69 65 70 75 80

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71 tta ccc aaa gct cct cca ctc cgg gaa ctg att gat cag tat gat gtc      346
72 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
73                               85                               90                               95
75 cag agg gat gac agc agc gat ggc tct ttg gaa gat gac gat tat cac      394
76 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
77                               100                              105                              110
79 gct aca acg qaa aca atc att acc atg cct aca gag tct gat ttt cta      442
80 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
81                               115                              120                              125
83 atg caa gtg gat gga aaa ccc aaa tgt tgc ttc ttt aaa ttt agc tct      490
84 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
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87 aaa ata caa tac aat aaa gta gta aaq gcc caa cta tgg ata tat ttg      538
88 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
89 145                               150                              155                              160
91 aga ccc gtc gaq act cct aca aca gtg ttt gtg caa atc ctg aga ctc      586
92 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
93                               165                              170                              175
95 atc aaa cct atg aaa gac ggt aca agg tat act gga atc cga tct ctg      634
96 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
97                               180                              185                              190
99 aaa ctt gac atg aac cca ggc act ggt att tgg cag agc att gat gtg      682
100 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
101                               195                              200                              205
103 aag aca qtg ttg caa aat tgg ctc aaa caa cct qaa tcc aac tta ggc      730
104 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
105                               210                              215                              220
107 att gaa ata aaa gct tta gat gag aat ggt cat gat ctt gct gta acc      778
108 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
109 225                               230                              235                              240
111 ttc cca gga cca gga gaa gat ggg ctg aat ccg ttt tta gag gtc aag      826
112 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
113                               245                              250                              255
115 gta aca gac aca cca aaa aga tcc aga agg gat ttt ggt ctt gac tgt      874
116 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
117                               260                              265                              270
119 gat gag cac tca aca gaa tca cga tgc tgt cgt tac cct cta act gtg      922
120 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
121                               275                              280                              285
123 gat ttt gaa gct ttt gga tgg gat tgg att atc gct cct aaa aga tat      970
124 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
125                               290                              295                              300
127 aag gcc aat tac tgc tct gga gag tgt gaa ttt gta ttt tta caa aaa      1018
128 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
129 305                               310                              315                              320
131 tat cct cat act cat ctg gta cac caa gca aac ccc aga ggt tca gca      1066
132 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
133                               325                              330                              335
135 ggc cct tgc tgt act ccc aca aag atg tct cca att aat atg cta tat      1114

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136 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
137          340          345          350
139 ttt aat ggc aaa gaa caa ata ata tat ggg aaa att cca gcg atg gta      1162
140 Phe Asn Gly Lys Glu Gln ile ile Tyr Gly Lys Ile Pro Ala Met Val
141          355          360          365
143 gta gac cgc tgt ggg tgc tca tgagatttat attaagcgtt cataacttcc      1213
144 Val Asp Arg Cys Gly Cys Ser
145          370          375
147 raaaacatgg aaggttttcc cctcaacaat tttgaagctg tgaaattaag taccacaggc      1273
149 tataggccta gagtatgcta cagtcactta agcataagct acagtatgta aactaaaagg      1333
151 gggaatatat gcaatgggtt gcatttaacc alccaaacaa atcatacaag aaagttttat      1393
153 gatttccaga gtttttqagc tagaaggaga tcaaattaca tttatgttcc tatatattac      1453
155 aacatcgccg aggaaatgaa agcgattctc cttgagttct gatgaattaa aggagtatgc      1513
157 tttaaagtct atttctttta agttttgttt aatattttaca gaaaaatcca catacagtat      1573
159 tggtaaaatg caggattgtt atataccatc attcgaatca tctctaaaca cttgaattta      1633
161 tattgtatgg tagtatactt qgtaagataa aatccacaa aaatagggat ggtgcagcat      1693
163 atgcaatttc cattctattt ataattgaca cagtacatta acaatccatg ccaacggtgc      1753
165 taatacgate ggcgaatgtt ctgaggctac caggttttat acataaaaaa cattcaqtaa      1813
167 aatagtaagt ttctcttttc ttccaggtgca ttttcttaca cctccaaatg aggaatggat      1873
169 tttctttaat gtaagaagaa tcatttttct agaggttggc tttcaattct gtgcatact      1933
171 tggagaaact gattatctt aaaaggcagt caaatgggtt ttgtttttat caaatgtca      1993
173 aaataacata cttggagaag katgtaattt tgtctttgga aaattacaac actgcctttg      2053
175 caacactgca gtttttatgg taaaataata gaaatgatcg actctatcaa tattgtataa      2113
177 aaagactgaa acaatgcatt tatataatat gtatacaata ttgttttgta aataagtgtc      2173
179 tctcttttta ttacttttgg tatattttta cactaaggac atttcaaatt aagtactaaq      2233
181 gcacaaagac atgtcatgca tcacagaaaa gcaactactt atatttcaga gcaaattagc      2293
183 agattaaata gtggtcttaa aactccatat gttaatgatt agatgggtat attacaatca      2353
185 ttttatattt ttttacatga ttaacattca cttatggatt catgatggct gtataaagtq      2413
187 aatttgaaat ttcaatgggt tactgtcatt gtgttttaaat ctcaacgttc cattatttta      2473
189 atacttgcaa aaacattact aagtatacca aaataattga ctctattatc tgaaatgaag      2533
191 aataaactga tgcattctca acaataactg ttacttttat ttataaattt gataatgaat      2593
193 atatttctgc atttatttac ttctgttttg taaattggga ttttgtaat caaatttatt      2653
195 gtactatgac taaatgaaat tatttcttac atctaatttg tagaaacagt ataagttata      2713
197 ttaaagtgtt ttcacatttt ttgaaagac      2743
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201 <211> LENGTH: 375
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 2
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212          20          25          30
215 Val Glu Lys Glu Gly Leu Cys Asn Ala Cys Thr Trp Arg Gln Asn Thr
216          35          40          45
219 Lys Ser Ser Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu
220          50          55          60
223 Arg Leu Glu Thr Ala Pro Asn Ile Ser Lys Asp Val Ile Arg Gln Leu
224 65          70          75          80

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227 Leu Pro Lys Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val
228                85                90                95
231 Gln Arg Asp Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His
232                100                105                110
235 Ala Thr Thr Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu
236                115                120                125
239 Met Gln Val Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser
240                130                135                140
243 Lys Ile Gln Tyr Asn Lys Val Val Lys Ala Gln Leu Trp Ile Tyr Leu
244 145                150                155                160
247 Arg Pro Val Glu Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu
248                165                170                175
251 Ile Lys Pro Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu
252                180                185                190
255 Lys Leu Asp Met Asn Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val
256                195                200                205
259 Lys Thr Val Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly
260                210                215                220
263 Ile Glu Ile Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr
264 225                230                235                240
267 Phe Pro Gly Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys
268                245                250                255
271 Val Thr Asp Thr Pro Lys Arg Ser Arg Arg Asp Phe Gly Leu Asp Cys
272                260                265                270
275 Asp Glu His Ser Thr Glu Ser Arg Cys Cys Arg Tyr Pro Leu Thr Val
276                275                280                285
279 Asp Phe Glu Ala Phe Gly Trp Asp Trp Ile Ile Ala Pro Lys Arg Tyr
280                290                295                300
283 Lys Ala Asn Tyr Cys Ser Gly Glu Cys Glu Phe Val Phe Leu Gln Lys
284 305                310                315                320
287 Tyr Pro His Thr His Leu Val His Gln Ala Asn Pro Arg Gly Ser Ala
288                325                330                335
291 Gly Pro Cys Cys Thr Pro Thr Lys Met Ser Pro Ile Asn Met Leu Tyr
292                340                345                350
295 Phe Asn Gly Lys Glu Gln Ile Ile Tyr Gly Lys Ile Pro Ala Met Val
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300                370                375
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304 <211> LENGTH: 2676
305 <212> TYPE: DNA
306 <213> ORGANISM: Mus musculus
308 <220> FEATURE:
309 <221> NAME/KEY: CDS
310 <222> LOCATION: (104)..(1231)
312 <400> SEQUENCE: 3
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315 aaataagaac aagggaataa aaaagattgt gctgattttt aaa atg atg caa aaa      115
316                               Met Met Gln Lys

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317                                     1
319 ctg caa atg tat gtt tat att tac ctg ttc atg ctg att gct gct ggc      163
320 Leu Gln Met Tyr Val Tyr Ile Tyr Leu Phe Met Leu Ile Ala Ala Gly
321 5                                10                                15                                20
323 cca gtg gat cta aat gag ggc agt gag aga gaa aat gtg gaa aaa      211
324 Pro Val Asp Leu Asn Glu Gly Ser Glu Arg Glu Glu Asn Val Glu Lys
325                                25                                30                                35
327 gag ggg ctg tgt aat gca tgt gcg tgg aga caa aac acg agg tac tcc      259
328 Glu Gly Leu Cys Asn Ala Cys Ala Irp Arg Gln Asn Thr Arg Tyr Ser
329                                40                                45                                50
331 aga ata gaa gcc ata aaa att caa atc ctg agt aag ctg cgc ctg gaa      307
332 Arg Ile Glu Ala Ile Lys Ile Gln Ile Leu Ser Lys Leu Arg Leu Glu
333                                55                                60                                65
335 aca gct cct aac atc agc aaa gat gct ata aga caa ctt ctg cca aga      355
336 Thr Ala Pro Asn Ile Ser Lys Asp Ala Ile Arg Gln Leu Leu Pro Arg
337                                70                                75                                80
339 gcg cct cca ctg cgg gaa ctg atc gat cag tac qac gtc cag agg gat      403
340 Ala Pro Pro Leu Arg Glu Leu Ile Asp Gln Tyr Asp Val Gln Arg Asp
341 85                                90                                95                                100
343 gac agc agt gat ggc tct ttg qaa gat qac gat tat cac gct acc acg      451
344 Asp Ser Ser Asp Gly Ser Leu Glu Asp Asp Asp Tyr His Ala Thr Thr
345                                105                                110                                115
347 gaa aca atc att acc atg cct aca gag tct qac ttt cta atg caa gcg      499
348 Glu Thr Ile Ile Thr Met Pro Thr Glu Ser Asp Phe Leu Met Gln Ala
349                                120                                125                                130
351 gat ggc aag ccc aaa tgt tgc ttt ttt aaa ttt agc tct aaa ata cag      547
352 Asp Gly Lys Pro Lys Cys Cys Phe Phe Lys Phe Ser Ser Lys Ile Gln
353                                135                                140                                145
355 tac aac aaa gta gta aaa gcc caa ctg tgg ata tat ctg aga ccc gtc      595
356 Tyr Asn Lys Val Val Lys Ala Gln Leu Irp Ile Tyr Leu Arg Pro Val
357                                150                                155                                160
359 aag act cct aca aca gtg ttt ttg caa atc ctg aga ctg atc aaa ccc      643
360 Lys Thr Pro Thr Thr Val Phe Val Gln Ile Leu Arg Leu Ile Lys Pro
361 165                                170                                175                                180
363 atg aaa gac ggt aca agg tat act gga atc cga tct ctg aaa ctt gac      691
364 Met Lys Asp Gly Thr Arg Tyr Thr Gly Ile Arg Ser Leu Lys Leu Asp
365                                185                                190                                195
367 atg agc cca ggc act ggt att tgg cag agt att gat gtg aag aca gtg      739
368 Met Ser Pro Gly Thr Gly Ile Trp Gln Ser Ile Asp Val Lys Thr Val
369                                200                                205                                210
371 ttg caa aat tgg ctg aaa cag cct gaa tcc aac tta ggc att gaa atc      787
372 Leu Gln Asn Trp Leu Lys Gln Pro Glu Ser Asn Leu Gly Ile Glu Ile
373                                215                                220                                225
375 aaa gct ttg gat gag aat ggc cat gat ctt gct gta acc ttc cca gga      835
376 Lys Ala Leu Asp Glu Asn Gly His Asp Leu Ala Val Thr Phe Pro Gly
377                                230                                235                                240
379 cca gga gaa gat ggg ctg aat ccc ttt tta gaa gtc aag gtg aca gac      883
380 Pro Gly Glu Asp Gly Leu Asn Pro Phe Leu Glu Val Lys Val Thr Asp
381 245                                250                                255                                260

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PSI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
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Input Set : A:\JHU1120-15.ST25.txt
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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21